Amendments to the specification:

Please replace the paragraph beginning on page 6, line 15, with the following amended paragraph:

Another aspect of the present invention provides a method of determining a portion of a genome of an organism that is responsive to a perturbation. In this aspect of the present invention, a first phenotypic data structure is produced that represents a difference in a first phenotype between different strains of the organism. The first phenotype is measured for each of the different strains of the organism when each different strain is in a first state. Then, a genotypic data structure is established. The genotypic data structure corresponds to a locus selected from a plurality of loci within the genome of the organism. Further, the genotypic data structure represents a variation, between different strains of the organism, of at least one component of the selected locus. The first phenotypic data structure is compared to the genotypic data structure to form a correlation value. These establishing and comparing steps are repeated for each locus in the plurality of loci. In this way a first set of genotypic data structures is identified ~~thats~~ that form a high correlation value relative to all other genotypic data structures evaluated in iterations of the comparing step.

Please replace the paragraph beginning on page 16, line 5, with the following amended paragraph:

In processing step 206, a genotypic data structure is established for the selected locus. In one embodiment, processing step 206 is performed by genotypic data structure derivation subroutine 48 (FIG. 1). The genotypic data structure is typically formed ~~in~~ by a method similar to the construction of the phenotypic data structure. The values of the phenotypic data structure are typically the differences in quantitative traits exhibited by several strains of an organism of interest. In contrast, the values in the genotypic data structure correspond to counts of the polymorphic differences between strains for a given locus L that contains M genetic variations, such as SNPs. That is, a given locus L may have several independent genetic variations M, and the goal of the genotypic array that corresponds to this locus is to quantify the number of these independent genetic variations. To accomplish this, an individual variation matrix S^x is established for each variation in every position **x** within

locus *L*. In each such matrix, S^x, the i^{th} row and the j^{th} column are associated with the allele value $l^x(i)$ for strain i and the allele value $l^x(j)$ for strain j at locus position **x** according to the following rule:

$$S^x(i, j) = 1/2 \text{ if } l^x(i) = \varnothing \text{ or } l^x(j) = \varnothing$$
$$= 0 \text{ if } l^x(i) = l^x(j)$$
$$= 1 \text{ if } l^x(i) \neq l^x(j)$$

where $\varnothing$ indicates the allelic value for strain i at locus position **x** is not known at the present time. Therefore, if the alleles for two strains i and j are identical at position **x**, the entry in the individual variation matrix for **x** would be:

$$S^x(i, j) = S^x(j, i) = 0$$

and if the two alleles are different, a "1" is entered.